

RAW SEQUENCE LISTING

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Application Serial Number: 10/540,971
Source: PCT
Date Processed by STIC: 7-11-05

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,971

DATE: 07/11/2005
TIME: 15:05:25

Input Set : A:\01640393aa.txt
Output Set: N:\CRF4\07112005\J540971.raw

3 <110> APPLICANT: Whaley, Cory M.
 4 Wilson, Henry P.
 5 Westwood, James H.
 7 <120> TITLE OF INVENTION: Gene Encoding Resistance to Acetolactate Synthase-Inhibiting
 8 Herbicides
 10 <130> FILE REFERENCE: 01640393aa
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/540,971
 C--> 12 <141> CURRENT FILING DATE: 2005-06-27
 12 <150> PRIOR APPLICATION NUMBER: US 60/438,801
 13 <151> PRIOR FILING DATE: 2003-01-09
 15 <150> PRIOR APPLICATION NUMBER: PCTUS04/00363
 16 <151> PRIOR FILING DATE: 2004-01-09
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1846
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Amaranthus hybridus
 27 <400> SEQUENCE: 1
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 32 cccagaaaag gttgcgtatgt tctcggtgaa gctcttgaac gtgaagggtgt taccgatgtt 180
 34 tttgcttacc ctgggtggagc atccatggaa attcatcaag ctcttactcg ttctaatatc 240
 36 attagaaaatg ttcttcctcg acatgaaccaa ggtggggttt tcgctgctga aggctacgct 300
 38 cgtgctactg gacgcgttgg agtttgtatt gccacttctg gtccaggtgc tactaatctt 360
 40 gtttctggtc ttgctgtatgc acttcttgac tcagtcctc ttgtcgccat tactgggcaa 420
 42 gttccccggc gtatgattgg tactgatgct tttcaagaga ctccaattgt tgaggttaact 480
 44 cgatccatta ccaagcataa ttatttgggt ttagatgttgg aggatattcc tagaattgtt 540
 46 aaggaagctt tctttttagc taattctggt agacctggac ctgtttgtat tgatattcct 600
 48 aaagatattc agcaacaatt agttgttccct aattgggaac agcccattaa attgggtggg 660
 50 tatctttcta ggtgcctaa acccacttat tctgctaattg aagagggaact tcttgatcaa 720
 52 attgtaaggt tagtgggtga gtcataagaga cctgtgtgt atactggagg tgggtgtttg 780
 54 aattctagtg aagaatttgag gaaatttgc gaatttgcacag gtattccgtt ggctagtact 840
 56 ttaatgggtt tgggggcttt cccttgcact gatgatttat ctcttcatat gttgggaatg 900
 58 cacgggactg tgtacgcgaa ttacgcggt gataaggccg atttgggtgt tgctttggg 960
 60 gttagggtt atgaacgagt gactggtaag ctcgaggcgt ttgctagccg ggctaaagatt 1020
 62 gtgcacatcg atatcgattc tgctgaaatc gggagaata agcaacctca tgtgtcgatt 1080
 64 tgtgggtatg ttaaagtggc attacagggg ttgaataaga ttttggaaatc tagaaaagga 1140
 66 aaggtgaaat tggatttctc taattggagg gaggagttga atgagcagaa aaagaagttt 1200
 68 cctttgagtt ttaagacttt cggggatgca attccctccgc aatacgcctt tcaggttctt 1260
 70 gacgagttga cgaaggcga tgcgggttgc agtactggg ttgggcagca ccaaattgtgg 1320
 72 gctgcccatt tctataagta cggaaatcc tgcgcatttgc tgacctcggtt gggtttgggg 1380
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76 gttgttagaca ttgatgggga tgggagttt atcatgaatg ttcaagagtt ggctacgatt 1500
 78 aggtagaga atctcccggt taaaatcatg ctcttgaaca atcaacattt aggtatggtt 1560
 80 gttcaatggg aagatcgatt ttacaaagct aaccgggcac atacatacct cgggaatcct 1620
 82 tccaaattctt ccgaaatctt cccggatatg ctcaaattt ctgaagcatg tcatatacca 1680
 84 gcagcccggt ttaccaaggt gagcgattt aaggctgcaa ttcaaacaat gttggatact 1740
 86 ccaggaccgt atctgctgga tptaatcgta ccacatcagg agcatgtgct gcctatgatc 1800
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 92 <211> LENGTH: 614
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 94 <213> ORGANISM: Amaranthus hybridus
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 102 Thr Gln Ser Pro Ser Ser Leu Thr Asp Asp Lys Pro Ser Ser Phe Val
 103 20 25 30
 106 Ser Arg Phe Ser Pro Glu Glu Pro Arg Lys Gly Cys Asp Val Leu Val
 107 35 40 45
 110 Glu Ala Leu Glu Arg Glu Gly Val Thr Asp Val Phe Ala Tyr Pro Gly
 111 50 55 60
 114 Gly Ala Ser Met Glu Ile His Gln Ala Leu Thr Arg Ser Asn Ile Ile
 115 65 70 75 80
 118 Arg Asn Val Leu Pro Arg His Glu Gln Gly Gly Val Phe Ala Ala Glu
 119 85 90 95
 122 Gly Tyr Ala Arg Ala Thr Gly Arg Val Gly Val Cys Ile Ala Thr Ser
 123 100 105 110
 126 Gly Pro Gly Ala Thr Asn Leu Val Ser Gly Leu Ala Asp Ala Leu Leu
 127 115 120 125
 130 Asp Ser Val Pro Leu Val Ala Ile Thr Gly Gln Val Pro Arg Arg Met
 131 130 135 140
 134 Ile Gly Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val Thr Arg
 135 145 150 155 160
 138 Ser Ile Thr Lys His Asn Tyr Leu Val Leu Asp Val Glu Asp Ile Pro
 139 165 170 175
 142 Arg Ile Val Lys Glu Ala Phe Phe Leu Ala Asn Ser Gly Arg Pro Gly
 143 180 185 190
 146 Pro Val Leu Ile Asp Ile Pro Lys Asp Ile Gln Gln Gln Leu Val Val
 147 195 200 205
 150 Pro Asn Trp Glu Gln Pro Ile Lys Leu Gly Gly Tyr Leu Ser Arg Leu
 151 210 215 220
 154 Pro Lys Pro Thr Tyr Ser Ala Asn Glu Glu Gly Leu Leu Asp Gln Ile
 155 225 230 235 240
 158 Val Arg Leu Val Gly Glu Ser Lys Arg Pro Val Leu Tyr Thr Gly Gly
 159 245 250 255
 162 Gly Cys Leu Asn Ser Ser Glu Glu Leu Arg Lys Phe Val Glu Leu Thr
 163 260 265 270
 166 Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly Ala Phe Pro Cys
 167 275 280 285
 170 Thr Asp Asp Leu Ser Leu His Met Leu Gly Met His Gly Thr Val Tyr

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171	290	295	300	
174	Ala Asn Tyr Ala Val Asp Lys Ala Asp Leu Leu Leu Ala Phe Gly Val			
175	305	310	315	320
178	Arg Phe Asp Glu Arg Val Thr Gly Lys Leu Glu Ala Phe Ala Ser Arg			
179	325	330	335	
182	Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu Ile Gly Lys Asn			
183	340	345	350	
186	Lys Gln Pro His Val Ser Ile Cys Gly Asp Val Lys Val Ala Leu Gln			
187	355	360	365	
190	Gly Leu Asn Lys Ile Leu Glu Ser Arg Lys Gly Lys Val Lys Leu Asp			
191	370	375	380	
194	Phe Ser Asn Trp Arg Glu Glu Leu Asn Glu Gln Lys Lys Lys Phe Pro			
195	385	390	395	400
198	Leu Ser Phe Lys Thr Phe Gly Asp Ala Ile Pro Pro Gln Tyr Ala Ile			
199	405	410	415	
202	Gln Val Leu Asp Glu Leu Thr Lys Gly Asp Ala Val Val Ser Thr Gly			
203	420	425	430	
206	Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr Lys Tyr Arg Asn			
207	435	440	445	
210	Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu Gly Ala Met Gly Phe Gly			
211	450	455	460	
214	Leu Pro Ala Ala Ile Gly Ala Ala Val Ala Arg Pro Asp Ala Val Val			
215	465	470	475	480
218	Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn Val Gln Glu Leu			
219	485	490	495	
222	Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Ile Met Leu Leu Asn			
223	500	505	510	
226	Asn Gln His Leu Gly Met Val Val Gln Trp Glu Asp Arg Phe Tyr Lys			
227	515	520	525	
230	Ala Asn Arg Ala His Thr Tyr Leu Gly Asn Pro Ser Asn Ser Ser Glu			
231	530	535	540	
234	Ile Phe Pro Asp Met Leu Lys Phe Ala Glu Ala Cys Asp Ile Pro Ala			
235	545	550	555	560
238	Ala Arg Val Thr Lys Val Ser Asp Leu Arg Ala Ala Ile Gln Thr Met			
239	565	570	575	
242	Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile Val Pro His Gln			
243	580	585	590	
246	Glu His Val Leu Pro Met Ile Pro Ser Gly Ala Ala Phe Lys Asp Thr			
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254	<210> SEQ ID NO: 3			
255	<211> LENGTH: 1930			
256	<212> TYPE: DNA			
257	<213> ORGANISM: Amaranthus hybridus			
259	<400> SEQUENCE: 3			
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264	cccgaaaaag gttgcgtatgt tctcggtt gaa gctcttgaac gtgaagggtgt taccgtatgtt			180

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270	cgtgctactg	gacgcgttgg	agtttgtatt	gccacttctg	gtccagggtgc	tactaatctt	360
272	gtttctggtc	ttgctgatgc	acttcttgc	tcagtccctc	ttgtcgccat	tactgggcaa	420
274	gttccccggc	gtatgattgg	tactgatgt	tttcaagaga	ctccaattgt	tgaggttaact	480
276	cgtatccatta	ccaagcataa	ttatttggtg	ttagatgtt	agatattcc	tagaattgtt	540
278	aaggaaagctt	tctttttagc	taattctgg	agacctggac	ctgttttgat	tgatattcct	600
280	aaaagatattc	agcaacaatt	agttgttcc	aattgggaa	agcccattaa	attgggtggg	660
282	tatcttcta	ggttgcctaa	accacttat	tctgcta	aagaggact	tcttgatcaa	720
284	attgtaaagg	tagtgggtga	gtctaaagaga	cctgtgt	atactggagg	tgggtgttt	780
286	aattcttagt	aagaattgag	gaaatttgc	gaatgtacag	gtattccgg	ggctagtagact	840
288	ttaatgggt	tggggctt	ccctgtact	gatgattat	ctcttcatat	gttggaaatg	900
290	cacgggactg	tgtacgcgaa	ttacgcgg	gataaggccg	atttgggt	tgcttttggg	960
292	gttaggttt	atgatcgagt	gactggtaag	ctcgaggcgt	ttgctagccg	ggctaagatt	1020
294	gtgcacatcg	atatcgattc	tgctgaaatc	gggaagaata	agcaacatca	tgtgtcgatt	1080
296	tgtggtgatg	ttaaagtggc	attacagggg	ttgaataaga	ttttggaaatc	tagaaaagga	1140
298	aaggtgaaat	tggatttctc	taattggagg	gaggagtga	atgagcagaa	aaagaagtt	1200
300	cctttgagtt	ttaagacttt	cggggatgca	attcctccgc	aatacgccat	tcaagttctt	1260
302	gacgagttga	cgaagggcga	tgcgggttga	agta	ttgggcagca	ccaaatgtgg	1320
304	gctgccaat	tctataagta	ccgaaatcct	cgccaaatggc	tgacctcggg	tgggttggg	1380
306	gctatgggt	ttggcttacc	agctgtt	ggagctgt	ttgctcgacc	agatgcgg	1440
308	gtttagaca	ttgatgggg	tggagttt	atcatgaatg	ttcaagagtt	ggctacgatt	1500
310	aggtagaga	atctccgg	taaaatcatg	ctcttgaaca	atcaacat	aggatgttt	1560
312	gttcaatggg	aagatcgatt	ttacaaagct	aaccgggcac	atacatacct	cgggaaatcct	1620
314	tccaaattctt	ccgaaatctt	cccggatatg	ctcaaattt	ctgaagcatg	tgatatacca	1680
316	gcagcccgt	ttaccaaggt	gagcattt	aggctgc	ttcaaacaat	gttggatact	1740
318	ccaggaccgt	atctgcttga	tgtatcgta	ccacatcagg	agcatgtgt	gcctatgtatc	1800
320	cctagcgggt	ccgccttcaa	ggacaccata	acagagggt	atgaaagaag	ggcttattag	1860
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327 <210> SEQ ID NO: 4

328 <211> LENGTH: 619

329 <212> TYPE: PRT

330 <213> ORGANISM: Amaranthus hybridus

332 <400> SEQUENCE: 4

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339					20			25				30				
342	Val	Ser	Arg	Phe	Ser	Pro	Glu	Glu	Pro	Arg	Lys	Gly	Cys	Asp	Val	Leu
343					35			40			45					
346	Val	Glu	Ala	Leu	Glu	Arg	Glu	Gly	Val	Thr	Asp	Val	Phe	Ala	Tyr	Pro
347					50			55			60					
350	Gly	Gly	Ala	Ser	Met	Glu	Ile	His	Gln	Ala	Leu	Thr	Arg	Ser	Asn	Ile
351					65			70			75					80
354	Ile	Arg	Asn	Val	Leu	Pro	Arg	His	Glu	Gln	Gly	Gly	Val	Phe	Ala	Ala
355								85			90					95
358	Glu	Gly	Tyr	Ala	Arg	Ala	Thr	Gly	Arg	Val	Gly	Val	Cys	Ile	Ala	Thr
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362 Ser Gly Pro Gly Ala Thr Asn Leu Val Ser Gly Leu Ala Asp Ala Leu
 363 115 120 125
 366 Asp Asp Ser Val Pro Leu Val Ala Ile Thr Gly Gln Val Pro Arg Arg
 367 130 135 140
 370 Met Ile Gly Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val Thr
 371 145 150 155 160
 374 Arg Ser Ile Thr Lys His Asn Tyr Leu Val Leu Asp Val Glu Asp Ile
 375 165 170 175
 378 Pro Arg Ile Val Lys Glu Ala Phe Phe Leu Ala Asn Ser Gly Arg Pro
 379 180 185 190
 382 Gly Pro Val Leu Ile Asp Ile Pro Lys Asp Ile Gln Gln Gln Leu Val
 383 195 200 205
 386 Val Pro Asn Trp Glu Gln Pro Ile Lys Leu Gly Gly Tyr Leu Ser Arg
 387 210 215 220
 390 Leu Pro Lys Pro Thr Tyr Ser Ala Asn Glu Glu Gly Leu Leu Asp Gln
 391 225 230 235 240
 394 Ile Val Arg Leu Val Gly Glu Ser Lys Arg Pro Val Leu Tyr Thr Gly
 395 245 250 255
 398 Gly Gly Cys Leu Asn Ser Ser Glu Glu Leu Arg Lys Phe Val Glu Leu
 399 260 265 270
 402 Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly Ala Phe Pro
 403 275 280 285
 406 Cys Thr Asp Asp Leu Ser Leu His Met Leu Gly Met His Gly Thr Val
 407 290 295 300
 410 Tyr Ala Asn Tyr Ala Val Asp Lys Ala Asp Leu Leu Ala Phe Gly
 411 305 310 315 320
 414 Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala Phe Ala Ser
 415 325 330 335
 418 Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu Ile Gly Lys
 419 340 345 350
 422 Asn Lys Gln Pro His Val Ser Ile Cys Gly Asp Val Lys Val Ala Leu
 423 355 360 365
 426 Gln Gly Leu Asn Lys Ile Leu Glu Ser Arg Lys Gly Lys Val Lys Leu
 427 370 375 380
 430 Asp Phe Ser Asn Trp Arg Glu Glu Leu Asn Glu Gln Lys Lys Lys Phe
 431 385 390 395 400
 434 Pro Leu Ser Phe Lys Thr Phe Gly Asp Ala Ile Pro Pro Gln Tyr Ala
 435 405 410 415
 438 Ile Gln Val Leu Asp Glu Leu Thr Lys Gly Asp Ala Val Val Ser Thr
 439 420 425 430
 442 Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr Lys Tyr Arg
 443 435 440 445
 446 Asn Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu Gly Ala Met Gly Phe
 447 450 455 460
 450 Gly Leu Pro Ala Ala Ile Gly Ala Ala Val Ala Arg Pro Asp Ala Val
 451 465 470 475 480
 454 Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn Val Gln Glu
 455 485 490 495
 458 Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Ile Met Leu Leu

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date